-continued

```
<210> SEQ ID NO 4
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse primer sequence
<400> SEQUENCE: 4
tgtatcgaat tccaagcaga ag
                                                                        22
<210> SEQ ID NO 5
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223 > OTHER INFORMATION: forward primer sequence
<400> SEQUENCE: 5
tetqteteet teetetteet aca
                                                                        23
<210> SEQ ID NO 6
<211> LENGTH: 19
<212> TYPE: DNA
<213 > ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse primer sequence
<400> SEQUENCE: 6
aaccagccct gtcgtctct
                                                                        19
<210> SEQ ID NO 7
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE
<223> OTHER INFORMATION: forward primer sequence
<400> SEQUENCE: 7
aatgatacgg cgaccaccga
                                                                        20
<210> SEQ ID NO 8
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<223> OTHER INFORMATION: reverse primer sequence
<400> SEQUENCE: 8
caagcagaag acggcatacg a
```

1.-38. (canceled)

- **39**. A method for sequencing double-stranded target nucleic acid molecules, comprising:
 - (a) ligating the double-stranded target nucleic acid molecules to double-stranded cyphers at both ends to form cypher-target nucleic acid complexes, wherein the double-stranded cyphers each comprise a random or partially random identifier sequence, and further wherein each target nucleic acid molecule is a DNA molecule comprising a target tag sequence that together with the double-stranded cyphers uniquely labels the double-stranded target nucleic acid molecule;
 - (b) amplifying each strand of the cypher-target nucleic acid complexes to produce a plurality of cypher-target

- amplification products from each of a first strand and a complementary second strand of the cypher-target nucleic acid complexes;
- (c) sequencing the cypher-target amplification products to produce a plurality of first-strand sequencing reads and a plurality of second-strand sequencing reads, wherein the plurality of first-strand sequencing reads and the plurality of second-strand sequencing reads each comprise an identifier sequence and a target tag sequence;
- (d) grouping the first-strand sequencing reads and secondstrand sequencing reads based on sequence identity of: the identifier sequence, and the target tag sequence,